CHLAMYDIA

No evidence of the Chlamydia trachomatis variant in the UK

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Objectives: The discovery of a variant strain of *Chlamydia trachomatis* (Ct) in Sweden has raised awareness of its possible undetected spread in the UK. The assays that fail to detect this variant are widely used in this country. This study aimed to determine if this variant is circulating in the UK.
Method: 1680 genital specimens tested negative by the Roche assays were retested by Aptima Combo2. Discordant results were sequenced to check for the deletion variant.
Results: Of 1680 specimens tested, 29 were candidates for sequencing: 16 were negative for the variant, 11 failed to amplify, and 2 were lost.
Discussion: No Ct deletion variants were found in the UK. If it is circulating, then the prevalence is low (0–0.77%), but even a low level cannot be ignored. The system we describe is simple and suitable for rapid response and phasing of surveillance to match an unknown level of threat if other variants emerge.

The discovery of a new variant *Chlamydia trachomatis* strain isolated in Sweden[1] and, more recently, in Norway[2] has caused some concern in the UK. To date, most detections of the variant outside Sweden—for example in Denmark and France—have been shown to have significant Swedish connections. It remains to be determined if this variant has been circulating undiagnosed here in England.

The Ct variant has a 377-bp deletion in the plasmid—a target area for the NAATs assays manufactured by Roche (Burgess Hill, UK) and Abbott, assays which between them are used in approximately a third of UK laboratories. These assays generate false-negative results in specimens from individuals infected with the variant. Other test platforms are unaffected, as they target different areas of chlamydia—two independent sequences of ribosomal RNA for Aptima Combo 2 (AC2) and Aptima CT (ACT) (Gen-Probe, San Diego, CA), an alternative plasmid sequence for Probetec (SDA) (Becton Dickinson) and a chromosomal sequence for RealArt CT (Artus).

As a pilot study, those laboratories using AC2 platform partnered with those using Roche platforms to survey the North and Midlands of the UK. Samples collected in the North had particular relevance, since many Scandinavians visit this area for the nightlife, facilitated by convenient direct ferry links.

METHODS

A total of 1680 specimens collected from genital sites and tested negative by the Roche Cobas or Taqman assay were retested by Aptima Combo 2, with reactive samples being confirmed by Aptima CT, a different target. All confirmed discrepant samples (Roche negative/Aptima positive) were sent to Malmo, Sweden for sequencing using a discriminatory assay to detect the Ct variant deletion (Kenneth Persson, to be published).

RESULTS

Of the 1680 specimens tested, 29 were found to be discrepant and were sent for sequencing (see table 1). Sixteen specimens tested positive for Ct in Sweden, but none were positive for the deletion variant.

DISCUSSION

There is no evidence that the variant has spread widely to other European countries.[3 4] To date, no Ct variants with the deletion have been detected in the UK.

In our study none of the 16 samples sequenced showed any evidence of the variant. However, 13 of 1680 specimens remain untested or unresolved. Failure to sequence 11 of these may be due to the assay and extraction process not being completely optimised or due to low organism load—PCR targets plasmid DNA (<10 copies per EB), and Aptima targets ribosomal RNA (~2000 copies per EB). Allowing for this uncertainty, if the variant is circulating in the UK, the prevalence is likely to be low, between 0% and 0.77%.

However, even a low level cannot be ignored. If the variant is present, and remains undetected and undiagnosed, it has the potential to continue to spread until it becomes a significant public health problem.

We recommend that continued enhanced surveillance, weighted to populations with a known connection to Sweden, should be performed while the ''failing'' widely used assays are reconfigured to be able to detect this mutant. The possibility that other variants may emerge should also be recognised, and assays detecting multiple targets should be used in surveillance. The system we have used here is simple and suitable for rapid response and phasing of surveillance to match an unknown level of threat if other variants emerge.

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Abbreviation: Ct, *Chlamydia trachomatis*

Table 1 Test results for the 1680 specimens

Roche PCR location	Tested by AC2 Liverpool or Norwich	Positive by AC2/ACT	Variant analysis findings Malmo, Sweden
Carlisle	376	4	1 tested and found to be negative for deletion variant
Newcastle	1017	18	13 tested and found to be negative for deletion variant
Preston	100	2	2 tested and found to be negative for deletion variant
Telford	187	5	All failed to amplify

REFERENCES

1 **Ripa T**, Nilsson P. A variant of *Chlamydia trachomatis* with deletion in cryptic plasmid: implications for use of the PCR diagnostic tests. *Eurosurveillance* 2006;**11**:E061109.2.
2 **Moghaddam A**, Reinton N. Identification of the Swedish *Chlamydia trachomatis* variant among patients attending a STI clinic in Oslo, Norway. *Eurosurveillance* 2007,12.3 (1.3.07).
3 **de Vries H**, Catsburg A, van der Helm J, Beukelaar E, Morre S, Fennema J, Thiesbrummel. No indication of Swedish *Chlamydia trachomatis* variant among STI clinic visitors in Amsterdam. *Eurosurveillance* 2007,12.2 (8.2.07).
4 **Lynagh Y**, Walsh A, Crowley B. Investigation to determine if newly-discovered variant of *Chlamydia trachomatis* is present in Ireland. *Eurosurveillance* 2007, 12.2 (1.2.07).